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GenCore version 5.1.6

protein - protein search, using sw model 1

on: December 27, 2004, 17:02:30 ; Search time 66.75 Seconds

(without alignment(s))

37.620 Million cell updates/sec

file: US-09-846-033B-36

sequence: 1 DRSNLTR 7

string table: OLIGO Gapop 60.0 , Gapext 60.0

searched: 2002273 seqs, 358729299 residues

word size : 7

total number of hits satisfying chosen parameters: 158

minimum DB seq length: 0

maximum DB seq length: 200000000

dt-processing: Listing first 45 summaries

No.	Score	Query Match Length	DB ID	Description
1	7	100.0	7 4 AAB84241	Aab84241 Zinc prot
2	7	100.0	7 5 ABB80798	Abb80798 Human ER-
3	7	100.0	7 5 ABP50162	Abp50162 Zinc finger
4	7	100.0	7 5 ABP50914	Abp50914 Zinc finger
5	7	100.0	7 5 ABP51092	Abp51092 Zinc finger
6	7	100.0	7 5 ABP50535	Abp50535 Zinc finger
7	7	100.0	7 5 ABP49313	Abp49313 Zinc finger
8	7	100.0	7 5 ABP50377	Abp50377 Zinc finger
9	7	100.0	7 5 ABP50373	Abp50373 Zinc finger
10	7	100.0	7 5 ABP48306	Abp48306 Zinc finger
11	7	100.0	7 5 ABP49231	Abp49231 Zinc finger
12	7	100.0	7 5 ABP49241	Abp49241 Zinc finger
13	7	100.0	7 5 ABP49259	Abp49259 Zinc finger
14	7	100.0	7 5 ABP49880	Abp49880 Zinc finger
15	7	100.0	7 5 ABP50861	Abp50861 Zinc finger
16	7	100.0	7 5 ABP50538	Abp50538 Zinc finger
17	7	100.0	7 5 ABP50920	Abp50920 Zinc finger
18	7	100.0	7 5 ABP50858	Abp50858 Zinc finger
19	7	100.0	7 5 ABP49274	Abp49274 Zinc finger
20	7	100.0	7 5 ABP50311	Abp50311 Zinc finger
21	7	100.0	7 5 ABP51150	Abp51150 Zinc finger
22	7	100.0	7 5 ABP49769	Abp49769 Zinc finger
23	7	100.0	7 5 ABP51159	Abp51159 Zinc finger
24	7	100.0	7 5 ABP51180	Abp51180 Zinc finger

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match Length	DB ID	Description
1	XX	XX	XX	RESULT 1
			ID AAB84241	standard; peptide; 7 AA.
			AC XX	
			DT XX	06-AUG-2001 (first entry)
			DE XX	Zinc protein recognition helix SBS9 for target DNA triplet GAC.
			KW XX	Phenotype associated gene; zinc finger protein; cancer; nephritis; prostate hypertrophy; hematopoiesis; osteoporosis; obesity; cardiovascular disease; diabetes.
			KW XX	
			OS XX	Synthetic.
			PS XX	
			PN XX	W0200140798-A2.
			PD XX	07-JUN-2001.
			PR XX	06-DEC-2000; 2000WO-US033086.
			PR XX	06-DEC-1999; 99US-00456100.
			PA XX	(SANG-) SANGMO BIOSCIENCES INC.
			PI XX	Caoe CC, Liu Q, Rebar EJ;
			DR XX	WPI; 2001-374953/39.
			XX	
			PT XX	Identifying genes associated with selected phenotype for research purposes, involves culturing cells transduced with nucleic acid encoding zinc finger proteins and assaying cells exhibiting selected phenotype.
			PT XX	
			PS XX	Example 1; Page 36; 58pp; English.
			PS XX	The specification describes a method for identifying genes associated with a selected phenotype. The method involves providing a library of nucleotide sequences encoding partially randomized zinc finger proteins, transducing cells with expression vectors, each comprising a sequence from the library, culturing the cells for expressing the zinc finger protein, assaying the cells for selected phenotype, and identifying the gene of interest, in cells exhibiting the phenotype. The method is useful for identifying a gene or genes associated with a selected phenotype such as the one related to cancer, nephritis, prostate hypertrophy, hematopoiesis, osteoporosis, obesity, cardiovascular disease or diabetes. The method is useful in academic laboratories, in the biotechnological industries, and in pharmaceutical, genomic, agricultural and chemical

ALIGNMENTS

CC companies. AAB84233-44 represent recognition helices of zinc finger
 CC proteins, which recognise different DNA triplets
 XX sequence 7 AA;
 SQ Query Match 100.0%; Score 7; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06; No. of Mismatches 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;
 QY 1 DRSNLTR 7
 Dp 1 DRSNLTR 7
 AC ABB80798;
 XX
 DT 23-SEP-2002 (first entry)
 XX Human ER-alpha locus targeting ZFP1 peptide #8.
 DE ZFP; cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin;
 KW gene expression; antirheumatic; antiarthritic; antipsoriatic; nootropic;
 KW neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;
 KW zinc finger protein.
 OS Synthetic.
 XX WO200244386-A2.
 PN 06-JUN-2002.
 PD XX
 PT 30-NOV-2001; 2001WO-US045098.
 PP XX
 DR PR 01-DEC-2000; 2000US-0250804P.
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX PT Wolfe AP, Tse C, Collingwood T;
 XX DR XX
 XX PR XX
 PT Regulating expression of gene by contacting cell with regulatory molecule
 PT comprising DNA-binding domain targeted to sequence within accessible
 PT region of cellular chromatin associated with a gene, and functional
 PT domain.
 XX PS Example 1; Page 44; 64pp; English.

XX The invention relates to regulating the expression of a gene residing in
 CC the chromatin of a cell. The method involves identifying one or more
 CC accessible regions in cellular chromatin associated with gene; designing
 CC a regulatory molecule, where the regulatory molecule comprises a DNA-
 CC binding domain targeted to a sequence within the accessible region, and a
 CC functional domain; and contacting the regulatory molecule with the cell.
 CC The method is used for regulating the expression of a gene (e.g., a gene
 CC encoding a nuclear receptor such as estrogen receptor alpha (ERalpha),
 CC estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha
 CC (HNF4Alpha), hepatocyte nuclear factor 4 gamma (HNF4Gamma), peroxisome
 CC proliferator activated receptor gamma (PPARgamma), retinoid X receptor
 CC alpha (RXRalpha), or constitutively active receptor alpha (CARalpha))
 CC residing in the chromatin of a cell. Regulation of gene expression (such
 CC as nuclear receptor genes) will be useful in treatment of various
 CC diseases, including cancer, diabetes and cardiovascular disease, where
 CC the regulatory molecule as described above, is contacted with the cell to
 CC carry out the regulation. The method is also useful for modulation of
 CC gene expression for therapeutic or prophylactic applications (e.g.,
 CC diabetic retinopathy, ischaemia, macular degeneration, rheumatoid
 CC arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's
 CC disease, stroke, etc. The method also has applications in pharmaceutical

CC research of both nuclear receptors of known function as well as those of
 CC unknown function. The method also facilitates development of tissue and
 CC animal models of disease states, drug validation, and therapeutic product
 CC development. The methods also allow identification of the role of nuclear
 CC receptors of unknown functions in cellular homeostasis. Sequences
 CC ABB80791-817 represent zinc finger protein (ZFP) DNA-binding domains that
 CC were fused to functional domains and tested for their ability to regulate
 CC expression of the ER in living cells
 SQ Sequence 7 AA;
 SQ Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06; No. of Mismatches 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;
 QY 1 DRSNLTR 7
 Dp 1 DRSNLTR 7
 AC ABB80812;
 XX
 DT 23-SEP-2002 (first entry)
 XX Human ER-alpha locus targeting ZFP3 peptide #4.
 DE ZFP; cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin;
 KW gene expression; antirheumatic; antiarthritic; antipsoriatic; nootropic;
 KW neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;
 KW zinc finger protein.
 OS Synthetic.
 XX WO200244386-A2.
 PN 06-JUN-2002.
 PD XX
 PT 30-NOV-2001; 2001WO-US045098.
 PP XX
 DR PR 01-DEC-2000; 2000US-0250804P.
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX PT Wolfe AP, Tse C, Collingwood T;
 XX DR XX
 XX PR XX
 PT Regulating expression of gene by contacting cell with regulatory molecule
 PT comprising DNA-binding domain targeted to sequence within accessible
 PT region of cellular chromatin associated with a gene, and functional
 PT domain.
 XX PS Example 1; Page 44; 64pp; English.
 XX The invention relates to regulating the expression of a gene residing in
 CC the chromatin of a cell. The method involves identifying one or more
 CC accessible regions in cellular chromatin associated with gene; designing
 CC a regulatory molecule, where the regulatory molecule comprises a DNA-
 CC binding domain targeted to a sequence within the accessible region, and a
 CC functional domain; and contacting the regulatory molecule with the cell.
 CC The method is used for regulating the expression of a gene (e.g., a gene
 CC encoding a nuclear receptor such as estrogen receptor alpha (ERalpha),
 CC estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha
 CC (HNF4Alpha), hepatocyte nuclear factor 4 gamma (HNF4Gamma), peroxisome
 CC proliferator activated receptor gamma (PPARgamma), retinoid X receptor
 CC alpha (RXRalpha), or constitutively active receptor alpha (CARalpha))
 CC residing in the chromatin of a cell. Regulation of gene expression (such
 CC as nuclear receptor genes) will be useful in treatment of various
 CC diseases, including cancer, diabetes and cardiovascular disease, where
 CC the regulatory molecule as described above, is contacted with the cell to
 CC carry out the regulation. The method is also useful for modulation of
 CC gene expression for therapeutic or prophylactic applications (e.g.,
 CC diabetic retinopathy, ischaemia, macular degeneration, rheumatoid
 CC arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's
 CC disease, stroke, etc. The method also has applications in pharmaceutical

the regulatory molecule as described above, is contacted with the cell to carry out the regulation. The method is also useful for modulation of gene expression for therapeutic or prophylactic applications e.g., diabetic retinopathy, ischaemia, macular degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's disease, stroke, etc. The method also has applications in pharmaceutical research of both nuclear receptors of known function as well as those of unknown function. The method also facilitates development of tissue and animal models of disease states, drug validation, and therapeutic product development. The methods also allow identification of the role of nuclear receptors of unknown functions in cellular homeostasis. Sequences ABB0791-817 represent zinc finger protein (ZFP) DNA-binding domains that were fused to functional domains and tested for their ability to regulate expression of the ER in living cells

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 7 AA:
||| | | | | | |

Qy 1 DRSNLTR 7
Db 1 DRSNLTR 7

RESULT 4
ABP50162
ID ABP50162 standard; peptide; 7 AA.
XX AC ABP50162;
XX DT 28-AUG-2002 (first entry)
XX DE Zinc finger protein related peptide motif SEQ ID NO:3466.
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2002A2459-A2.
XX PD 30-MAY-2002.
XX PR 20-NOV-2001; 2001WO-US043438.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI Liu Q;
XX DR WPI; 2002-500284/53.
XX PT New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
XX PS Example 1; Page 57; 81pp; English.

The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, selecting the F3 zinc finger such that it binds to the S3 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 7 AA:
||| | | | | | |

Qy 1 DRSNLTR 7
Db 1 DRSNLTR 7

RESULT 5
ABP50914
ID ABP50914 standard; peptide; 7 AA.
XX AC ABP50914;
XX DT 28-AUG-2002 (first entry)
XX DE Zinc finger protein related peptide motif SEQ ID NO:3417.
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2002A2459-A2.
XX PD 30-MAY-2002.
XX PR 20-NOV-2001; 2001WO-US043438.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI Liu Q;
XX DR WPI; 2002-500284/53.

New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.

Example 1; Page 62; 81pp; English.

The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid

useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ2214 and ABP48191 to ABP1230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 7 AA:
||| | | | | | |

Qy 1 DRSNLTR 7
Db 1 DRSNLTR 7

RESULT 5
ABP50914
ID ABP50914 standard; peptide; 7 AA.
XX AC ABP50914;
XX DT 28-AUG-2002 (first entry)
XX DE Zinc finger protein related peptide motif SEQ ID NO:3417.
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2002A2459-A2.
XX PD 30-MAY-2002.
XX PR 20-NOV-2001; 2001WO-US043438.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI Liu Q;
XX DR WPI; 2002-500284/53.

New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.

Example 1; Page 62; 81pp; English.

The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid

CC in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABPS1230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7
DB 1 DRSNLTR 7

RESULT 6
ABP51092
ID ABP51092 standard; peptide; 7 AA.
XX
AC ABP51092;
XX
DT 28-AUG-2002 (first entry)
DE Zinc finger protein related peptide motif SEQ ID NO:3976.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PP 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PT Liu Q;
XX
DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
XX
RS Example 1; Page 63; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M). (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (II) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABPS1230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.

CC finger peptides which are given in the exemplification of the present invention.
CC invention.
XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7
DB 1 DRSNLTR 7

RESULT 7
ABP5035
ID ABP5035 standard; peptide; 7 AA.
XX
AC ABP5035;
XX
DT 28-AUG-2002 (first entry)
DE Zinc finger protein related peptide motif SEQ ID NO:2791.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PT Liu Q;
XX
DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
XX
RS Example 1; Page 59; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M). (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (II) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABPS1230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.

CC Sequence 7 AA;

Query Match	100.0%	Score 7;	DB 5;	Length 7;	
Best Local Similarity	100.0%	Pred. No.	1.7e+06;		
Matches	7;	Conservative	0;	Mismatches	0;
Qy	1 DRSNLTR 7				
Db	1 DRSNLTR 7				
RESULT 8					
ID	ABP49313	Bstandard; peptide;	7 AA.		
XX					
AC	ABP49313;				
XX					
DT	28-AUG-2002 (first entry)				
XX					
DE	Zinc finger protein related peptide motif SBQ ID NO:1577.				
XX					
KW	Zinc finger protein; ZFP; DNA binding protein; zinc finger.				
XX					
OS	Homo sapiens.				
OS	Synthetic.				
XX					
PN	WO200242459-A2.				
XX					
PD	30-MAY-2002.				
XX					
PP	20-NOV-2001; 2001WO-US043438.				
XX					
PR	20-NOV-2000; 2000US-00716637.				
XX					
PA	(SANG-) SANGAMO BIOSCIENCES INC.				
XX					
PT	Liu Q;				
XX					
PS	WPI; 2002-500284/53.				
XX					
PT	New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.				
XX					
PS	Example 1; Page 48; 81pp; English.				
XX					
CC	The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ1213 to ABQ12214 and ABP41911 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention				
CC	Sequence 7 AA;				
XX					
CC	Query Match	100.0%	Score 7;	DB 5;	Length 7;
CC	Best Local Similarity	100.0%	Pred. No.	1.7e+06;	
CC	Matches	7;	Conservative	0;	Mismatches 0;
CC	Indels 0;	Gaps 0;			
Qy	1 DRSNLTR 7				
Db	1 DRSNLTR 7				
RESULT 9					
ID	ABP50277				
XX					
AC	ABP50277;				
XX					
DT	28-AUG-2002 (first entry)				
XX					
DE	Zinc finger protein related peptide motif SEQ ID NO:2705.				
XX					
KW	Zinc finger protein; ZFP; DNA binding protein; zinc finger.				
XX					
OS	Homo sapiens.				
OS	Synthetic.				
PN	WO200242459-A2.				
XX					
PD	30-MAY-2002.				
XX					
PF	20-NOV-2001; 2001WO-US043438.				
XX					
PR	20-NOV-2000; 2000US-00716637.				
XX					
PA	(SANG-) SANGAMO BIOSCIENCES INC.				
XX					
PI	Liu Q;				
XX					
DR	WPI; 2002-500284/53.				
XX					
PT	New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.				
XX					
PS	Example 1; Page 57; 81pp; English.				
XX					
CC	The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ1213 to ABQ12214 and ABP41911 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention				
CC	Sequence 7 AA;				
XX					
CC	Query Match	100.0%	Score 7;	DB 5;	Length 7;
CC	Best Local Similarity	100.0%	Pred. No.	1.7e+06;	
CC	Matches	7;	Conservative	0;	Mismatches 0;
CC	Indels 0;	Gaps 0;			
Qy	1 DRSNLTR 7				
Db	1 DRSNLTR 7				

RESULT 10
 ID ABP50373
 XX ABP50373 standard; peptide; 7 AA.
 AC ABP50373;
 XX DT 28-AUG-2002 (first entry)
 XX DE Zinc finger protein related peptide motif SEQ ID NO:2737.
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
 XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200242459-A2.
 XX PD 30-MAY-2002.
 XX PR 20-NOV-2001; 2001WO-US043438.
 XX PR 20-NOV-2000; 2000US-00716637.
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX PI Liu Q;
 XX DR WPI; 2002-500284/53.
 XX PT New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
 XX PS Example 1; Page 58; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ7123 to ABP7214 and ABP8191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention

XX Sequence 7 AA;
 SQ Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 ID ABP48386
 XX ABP48386;
 AC ABP48386;
 XX DT 28-AUG-2002 (first entry)
 XX DE Zinc finger protein related peptide motif SEQ ID NO:395.
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
 XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200242459-A2.
 XX PD 30-MAY-2002.
 XX PR 20-NOV-2001; 2001WO-US043438.
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX PI Liu Q;
 XX DR WPI; 2002-500284/53.
 XX PT New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
 XX PS Example 1; Page 37; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ7123 to ABP7214 and ABP8191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention

XX Sequence 7 AA;
 SQ Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 ID ABP49231
 XX ABP49231 standard; peptide; 7 AA.
 AC ABP49231;
 XX

DT 28-AUG-2002 (first entry)
 XX DE Zinc finger protein related peptide motif SEQ ID NO:1464.
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200242459-A2.
 XX PD 30-MAY-2002.
 XX PR 20-NOV-2001; 2001WO-US043438.
 XX PR 20-NOV-2000; 2000US-00716637.
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX PT New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises PT first, second and third zinc fingers, ordered from N- to C-terminus.
 XX PI Liu Q;
 XX DR WPI; 2002-500284/53.

PT The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus; where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite. (I) is useful for recognition of triplet target subsites (II) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (II) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (II) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in a sample, and in assays to determine the phenotype and function of diagnostic methods for sequence specific detection of target nucleic acid gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ1213 to ABQ1214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention

XX SQ Sequence 7 AA;

Query Match	Best Local Similarity	Score	DB	Length
1 DRSNLTR 7	100.0%;	7;	5;	7;
Matches	100.0%;	Pred. No.	1.7e+06;	
7; Conservative	0;	Mismatches	0;	Indels
		Oy	0;	Gaps
		Db	0;	0;

XX RESULT 13
 ABP49241 ID ABP49241 standard; peptide; 7 AA.
 AC ABP49241;
 XX DT 28-AUG-2002 (first entry)
 XX DE Zinc finger protein related peptide motif SEQ ID NO:1559.
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
 XX OS Homo sapiens.
 OS Synthetic.

XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200242459-A2.
 XX PD 30-MAY-2002.
 XX PR 20-NOV-2001; 2001WO-US043438.
 XX PR 20-NOV-2000; 2000US-00716637.
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX PT Liu Q;
 XX DR WPI; 2002-500284/53.

PT The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus; where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (II) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in a sample, and in assays to determine the phenotype and function of diagnostic methods for sequence specific detection of target nucleic acid gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ1213 to ABQ1214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention

XX SQ Sequence 7 AA;

Query Match	Best Local Similarity	Score	DB	Length
1 DRSNLTR 7	100.0%;	7;	5;	7;
Matches	100.0%;	Pred. No.	1.7e+06;	
7; Conservative	0;	Mismatches	0;	Indels
		Oy	0;	Gaps
		Db	0;	0;

XX RESULT 14
 ABP49259 ID ABP49259 standard; peptide; 7 AA.
 AC ABP49259;
 XX PT 28-AUG-2002 (first entry)
 XX DE Zinc finger protein related peptide motif SEQ ID NO:1559.
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
 XX OS Homo sapiens.
 OS Synthetic.

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OM protein - protein search, using SW model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds

Title: US-09-846-033B-36
Perfect score: 7
Sequence: 1 DRSNLTR 7Scoring table: OLIGO
Gapop 60.0 , Gapext: 60.0Searched: 478139 seqs, 66318000 residueB
Word size : 7Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 2: /cgpn2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgpn2_6/prodata/1/iaa/6A_COMB.pep:*
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- 5: /cgpn2_6/prodata/1/iaa/PCUTS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-20
2	7	100.0	27	4	US-09-424-487B-11
3	7	100.0	89	3	US-08-793-108-18
4	7	100.0	89	3	US-09-139-762A-18

ALIGNMENTS

RESULT 1	US-09-731-558-20					
; Sequence 20, Application US/09731558						
; Patent No. 6503717						
; CRNERIAL INFORMATION:						
; APPLICANT: Case, Casey Christopher						
; APPLICANT: Liu, Qiang						
; APPLICANT: Rebar, Edward J.						
; APPLICANT: Sangamo Biosciences, Inc.						
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger Proteins for the Identification of Gene Function						
; FILE REFERENCE: 019496-00210US						
; CURRENT APPLICATION NUMBER: US/09/731,558						
; CURRENT FILING DATE: 2000-12-06						
; PRIOR APPLICATION NUMBER: US 09/456,100						
; PRIOR FILING DATE: 1999-12-06						
; NUMBER OF SEQ ID NOS: 24						
; SOFTWARE: PatentIn Ver. 2.1						

RESULT 2
US-09-424-487B-11
Sequence 11, Application US/09424487B
Patent No. 6746838

GENERAL INFORMATION:

APPLICANT: CHOO, YEN
APPLICANT: KLUK, AARON
APPLICANT: ISALAN, MARK

TITLE OF INVENTION: NUCLEAR ACID BINDING PROTEINS

FILE REFERENCE: 71278/264975

CURRENT APPLICATION NUMBER: US/09/424,487B

CURRENT FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: GB 9710809.6

PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: PCT/GB98/01512

PRIOR FILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 11
LENGTH: 27

TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: Peptide
US-09-424-487B-11

RESULT 3
US-09-793-408-18
Sequence 18, Application US/08793408
Patent No. 6007988

GENERAL INFORMATION:

APPLICANT: CHOO, YEN
APPLICANT: KLUK, Aaron
APPLICANT: Sanchez Garcia, Isidro

TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793, 408
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422534. 9
FILING DATE: 08-NOV-1994
APPLICATION NUMBER: GB 9416880. 4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein

US-09-139-762A-18

Search completed: December 27, 2004, 18:12:04
Job time : 16.8 secs

Query Match 100.0%: Score 7: DB 3: Length 89

Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 7; Conservative 0; Indels 0; Gaps 0

Db 74 DRSNLTR 8

RESULT

US-09-139162A-18
; Sequence 18, Application US/09139762A
; Patent No. 6013453
; Grammar INNOVATION

APPLICANT: Choo, Yen
APPLICANT: Kluug, Aaron
APPLICANT: Sanchez Garcia, Tatiana

TITLE OF INVENTION: *Improvements in or Relating to Binding Proteins for Recognition of DNA*
NUMBER OF INVENTORS: 125

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.

STATE: D.C.
COUNTRY: USA

ZIP: 20005-3918
COMPUTER READABLE FORM:

MEDIUM TYPE: diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
PTI INC. DATE:

PRIOR APPLICATION DATA
CLASSIFICATION: FILING DATE:

APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: PCT/GB95/01944

FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995

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OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 seconds
(without alignments)
29.381 Million cell updates/sec

Title: US-09-846-033B-35
Perfect score: 7
Sequence: 1 RSDNLAR 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgnd_6/prodata/1/aa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-13
2	7	100.0	7	4	US-09-779-233-43

ALIGNMENTS

RESULT 1
US-09-731-558-13
; Sequence 13, Application US/09731558
; Patent No. 6503717
; GENERAL INFORMATION:
; APPLICANT: Case, Casey Christopher
; APPLICANT: Liu, Qiang
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger Proteins for the Identification of Gene Function
; FILE REFERENCE: 019436-002210US
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 09/456,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 7

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SBS2
US-09-731-558-13
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Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RSDNLAR 7
Oy 1 RSDNLAR 7
Dy 1 RSDNLAR 7

RESULT 2
US-09-779-233-43
; Sequence 43, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325.0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 43
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recognition
; OTHER INFORMATION: helix
US-09-779-233-43
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Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RSDNLAR 7
Oy 1 RSDNLAR 7
Dy 1 RSDNLAR 7

Search completed: December 27, 2004, 18:12:03
Job time : 15.8 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6		
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Maximum DB seq length:	2000000000		
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
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3	7	100.0	7 5 ABBB019
4	7	100.0	7 5 ABBB034
5	7	100.0	7 5 ABBP49764
6	7	100.0	7 5 ABP0067
7	7	100.0	7 5 ABP48642
8	7	100.0	7 5 ABP48552
9	7	100.0	7 5 ABP49518
10	7	100.0	7 5 ABP49797
11	7	100.0	7 5 ABP48621
12	7	100.0	7 5 ABP49260
13	7	100.0	7 5 ABP50082
14	7	100.0	7 5 ABP48649
15	7	100.0	7 5 ABP4794
16	7	100.0	7 5 ABP49110
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19	7	100.0	7 5 ABP49593
20	7	100.0	7 5 ABP5067
21	7	100.0	7 5 ABP4662
22	7	100.0	7 5 ABP49902
23	7	100.0	7 5 ABP48405
24	7	100.0	7 5 ABP50064
25	7	100.0	7 5 ABP50229

The invention relates to a method of screening a compound for interaction with a molecular target. The method involves contacting first and second cells with the compound and determining the values of properties of the compound. The second cell comprises an exogenous zinc finger protein (ZFP) that modulates the expression of the molecular target, or isolating membranes from cell comprising ZFP. The methods allow for high throughput screening of candidate compound and reduces the incidence of false positives. The methods are useful for screening a compound for interaction with a molecular target or for screening a compound for its effect on a cellular process. The method is useful for testing a compound for its capacity to transduce a signal to the molecular target or its capacity to block transduction of a signal through the molecular target,

CC and for performing biochemical drug-screening assays. The present
 CC sequence is human KC4 protein recognition helix used in the
 CC exemplification of the invention
 XX Sequence 7 AA:
 SQ Query Match 100.0%; Score 7; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OQ 1 RSDHLAR 7
 QV 1 RSDHLAR 7
 DB 1 RSDHLAR 7
 XX ABB80702;
 XX ABB80792;
 XX AC ABB80792;
 XX DT 23-SEP-2002 (first entry)
 DE Human ER-alpha locus targeting ZFP1 peptide #2.
 XX KW ZIP; cytosolic; antidiabetic; ophthalmological; vasotrophic; chromatin;
 KW gene expression; antiinflammatory; antipsoriatic; nocropic;
 KW neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;
 KW zinc finger protein.
 OS Synthetic.
 XX PN WO200244386-A2.
 XX PD 06-JUN-2002.
 XX PR 30-NOV-2001; 2001WO-US045098.
 XX PR 01-DEC-2000; 2000US-0250804P.
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX PI Wolfe AP, Tse C, Collingwood T;
 DR XX WPI; 2002-537455/57.
 XX PT Regulating expression of gene by contacting cell with regulatory molecule
 PT comprising DNA-binding domain targeted to sequence within accessible
 PT region of cellular chromatin associated with a gene, and functional
 PT domain.
 XX PS Example 1; Page 44; 64pp; English.
 XX CC The invention relates to regulating the expression of a gene residing in
 CC the chromatin of a cell. The method involves identifying one or more
 CC accessible regions in cellular chromatin associated with gene; designing
 CC a regulatory molecule, where the regulatory molecule comprises a DNA-
 CC binding domain targeted to a sequence within the accessible region, and a
 CC functional domain; and contacting the regulatory molecule with the cell.
 CC The method is used for regulating the expression of a gene (e.g., a gene
 CC encoding a nuclear receptor such as estrogen receptor alpha (ERalpha),
 CC estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha (HNF4alpha),
 CC (HNF4alphai), hepatocyte nuclear factor 4 gamma (HNF4gamma), peroxisome
 CC proliferator activated receptor gamma (PPARGamma), retinoid X receptor
 CC alpha (RXRalpha), or constitutively active receptor alpha (CARalpha))
 CC residing in the chromatin of a cell. Regulation of gene expression (such
 CC as nuclear receptor genes) will be useful in treatment of various
 CC diseases, including cancer, diabetes and cardiovascular disease, where
 CC the regulatory molecule as described above, is contacted with the cell to
 CC carry out the regulation. The method is also useful for modulation of
 CC gene expression for therapeutic or prophylactic applications e.g.,
 CC diabetic retinopathy, ischaemia, macular degeneration, rheumatoid
 CC arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's
 CC

CC disease, stroke, etc. The method also has applications in pharmaceutical
 CC research of both nuclear receptors of known function as well as those of
 CC unknown function. The method also facilitates development of tissue and
 CC animal models of disease states, drug validation, and therapeutic product
 CC development. The methods also allow identification of the role of nuclear
 CC receptors of unknown functions in cellular homeostasis. Sequences
 CC ABB80791-817 represent zinc finger protein (ZFP) DNA-binding domains that
 CC were fused to functional domains and tested for their ability to regulate
 CC expression of the ER in living cells
 XX Sequence 7 AA:
 SQ Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OQ 1 RSDHLAR 7
 QV 1 RSDHLAR 7
 DB 1 RSDHLAR 7
 XX ABB98019 standard; peptide: 7 AA.
 XX AC ABB98019;
 XX DT 06-SEP-2002 (first entry)
 DE Zinc finger protein 7 finger 1 peptide.
 XX KW Human; heparanase; cytosolic; vasotrophic; antidiabetic; anti-HIV;
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic;
 KW antianemic; neuroprotective; nocropic; cerebroprotective;
 KW antibacterial; virucide; protozoacide; fungicide; antiinflammatory;
 KW cardiot; immunosuppressive; tumour metastasis; inflammatory disease;
 KW allograft rejection; cell migration; angiogenesis; basement membrane;
 KW extracellular matrix; cancer; ischaemia; diabetic retinopathy;
 KW macular degeneration; rheumatoid arthritis; psoriasis; HIV infection;
 KW sickle cell anaemia; Alzheimer's disease; muscular dystrophy;
 KW neurodegenerative disease; vascular disease; cardiovascular disease;
 KW cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP.
 XX OS Homo sapiens.
 XX PN WO200244353-A2.
 XX PD 06-JUN-2002.
 XX PR 30-NOV-2001; 2001WO-US044798.
 XX PR 30-NOV-2000; 2000US-0250690P.
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX PI Wolfe AP, Qi H;
 DR XX WPI; 2002-527708/56.
 XX PT New heparanase polynucleotide, useful for controlling disease states such
 CC as tumor metastasis, inflammatory diseases and allograft rejection.
 XX Example 3; Page 49; 72pp; English.
 XX The invention relates to novel heparanase sequences, particularly novel
 CC sequences from the regulatory regions upstream and downstream of the
 CC coding region. The activity of polynucleotides of the invention may be
 CC described as, cytosolic, vasotrophic, antidiabetic, anti-HIV,
 CC ophthalmological, antiarthritic, antipsoriatic,
 CC antianemic, neuroprotective, nocropic, cerebroprotective,
 CC antibacterial, virucide, protozoacide, fungicide, antiinflammatory,
 CC cardiot; immunosuppressive. Modulating expression of heparanase gene
 CC using constructs of the invention is useful for facilitating targeted

CC	control of disease states such as tumour metastasis, inflammatory diseases, allograft rejection, and for inhibiting processes such as cell migration, angiogenesis, and degradation of the basement membrane and/or extracellular matrix. Heparanase-targeted DNA binding domains modulates gene expression, and are useful for therapeutic or prophylactic applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative diseases, vascular disease, cardiovascular disease, cystic fibrosis, stroke, and bacterial, protozoal, fungal and viral infection. Constructs of the invention may also be useful in gene therapy. The current sequence represents a finger of a three-finger ZFP (zinc finger protein), which has a target site in the human heparanase gene
XX	Sequence 7 AA;
SQ	
Query Match	100.0%; Score 7; DB 5; Length 7;
Best Local Similarity	100.0%; Pred. No. 1.7e+06;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Caps 0
Oy	1 RSDHAR 7
Db	1 RSDHAR 7
RESULT 4	
ID	ABB98034
DE	ABB98034 standard; peptide; 7 AA.
XX	
AC	ABB98034;
XX	
DT	06-SEP-2002 (first entry)
XX	
DB	Zinc finger protein 12 finger 1 peptide.
XX	
KW	Human; heparanase; cytostatic; vasoactive; antidiabetic; anti-HIV; ophthalmological; antibacterial; antiarthritic; antipsoriatic; antimicrobial; neuroprotective; nootropic; cerebroprotective; cardiotonic; virucide; protozoicide; fungicide; antiinflammatory; allograft; reflection; cell migration; angiogenesis; basement membrane; extracellular matrix; cancer; ischaemia; diabetic retinopathy; macular degeneration; rheumatoid arthritis; psoriasis; HIV infection; sickle cell anaemia; Alzheimer's disease; muscular dystrophy; neurodegenerative disease; vascular disease; cardiovascular disease; cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP. OX
XX	Homo sapiens.
PN	WO200244353-A2.
XX	
PD	06-JUN-2002.
XX	
PP	30-NOV-2001; 2001WO-US044798.
PR	30-NOV-2000; 2000US0-0250690P.
XX	
PA	(SANG-) SANGAMO BIOSCIENCES INC.
XX	
PI	Wolfe AP, Qi H;
XX	
DR	WPI; 2002-527708/56.
XX	
PT	New heparanase poly nucleotide, useful for controlling disease states such as tumor metastasis, inflammatory diseases and allograft rejection.
CC	The invention relates to novel heparanase sequences, particularly novel sequences from the regulatory regions upstream and downstream of the coding region. The activity of poly nucleotides of the invention may be described as, cyrostatic, vasoactive, antidiabetic, anti-HIV, ophthalmological, antirheumatic, antiarthritic, antipsoriatic,
CC	

CC antihaemetic, neuroprotective, nootropic, cerebroprotective,
CC antibacterial, virucide, protozoicide, fungicide, antiinflammatory,
CC cardiac and immunosuppressive. Modulating expression of heparanase gene
CC using constructs of the invention is useful for facilitating targeted
CC control of disease states such as tumour metastasis, inflammatory
CC diseases, allograft rejection, and for inhibiting processes such as cell
CC migration, angiogenesis, and degradation of the basement membrane and/or
CC extracellular matrix. Heparanase-targeted DNA binding domains modulates
CC gene expression, and are useful for therapeutic or prophylactic
CC applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular
CC degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell
CC anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative
CC diseases, vascular disease, cardiovascular disease, cystic fibrosis,
CC stroke, and bacterial, protozoal, fungal and viral infection. Constructs
CC of the invention may also be useful in gene therapy. The current sequence
CC represents a finger of a three-finger ZFP (zinc finger protein), which
CC has a target site in the human heparanase gene

CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention.

Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ Sequence 7 AA;

Qy	1 RSDHLAR 7
Db	1 RSDHLAR 7

RESULT 6

ID	ABP50057
AC	ABP50057;
XX	DT 28-AUG-2002 (first entry)
XX	DB Zinc finger protein related peptide motif SEQ ID NO:2635.
XX	KW zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX	OS Homo sapiens.
XX	OS Synthetic.
PN	WO200242459-A2.
PD	30-MAY-2002.
XX	PP 20-NOV-2001; 2001WO-US043438.
XX	PR 20-NOV-2000; 2000US-00716637.
XX	PA (SANG-) SANGAMO BIOSCIENCES INC.
XX	PT Liu Q;
XX	DR WPI; 2002-500284/53.
PT	New zinc finger protein that binds to target site, useful in studying PT gene function and for human therapeutics and plant engineering, comprises PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX	PS Example 1; Page 56; 81pp; English.
PT	The present invention describes a zinc finger protein (I) that binds to a PT target site, comprising a first (F1), a second (F2), and a third (F3) PT zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the PT target site comprises, in 3'-5' direction, a first (S1), a second (S2), PT and a third (S3) target subsite. Also described are: (1) a polypeptide XX (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it CC binds to the S1 target subsite, selecting the F2 zinc finger such that it CC binds to the S2 target subsite, and selecting the F3 zinc finger such CC that it binds to the S3 target subsite, thus designing (I) that binds to CC a target site. (I) is useful for recognition of triplet target subsites CC having the nucleotide G in the 5'-most position of the subsite. (I) is CC useful in studying gene function, and for human therapeutics and plant CC engineering. (I), (II) or (III) is useful in therapeutic methods to CC modulate the expression of a target region within a subject, in CC diagnostic methods for sequence specific detection of target nucleic acid CC in a sample, and in assays to determine the phenotype and function of CC gene expression. (I) has improved affinity and specificity for their CC target sequences, as well as enhanced biological activity. ABQ71213 to CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc CC finger peptides which are given in the exemplification of the present CC invention.

Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ Sequence 7 AA;

Qy	1 RSDHLAR 7
Db	1 RSDHLAR 7

RESULT 7

ID	ABP48642
AC	ABP48642;
XX	DT 28-AUG-2002 (first entry)
XX	DB Zinc finger protein related peptide motif SEQ ID NO:686.
XX	KW zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX	OS Homo sapiens.
XX	OS Synthetic.
PN	WO200242459-A2.
XX	PD 30-MAY-2002.
XX	PR 20-NOV-2001; 2001WO-US043438.
XX	PR 20-NOV-2000; 2000US-00716637.
XX	PA (SANG-) SANGAMO BIOSCIENCES INC.
XX	PT Liu Q;
XX	DR WPI; 2002-500284/53.
PT	New zinc finger protein that binds to target site, useful in studying PT gene function and for human therapeutics and plant engineering, comprises PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX	PS Example 1; Page 41; 81pp; English.
PT	The present invention describes a zinc finger protein (I) that binds to a PT target site, comprising a first (F1), a second (F2), and a third (F3) PT zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the PT target site comprises, in 3'-5' direction, a first (S1), a second (S2), PT and a third (S3) target subsite. Also described are: (1) a polypeptide XX (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it CC binds to the S1 target subsite, selecting the F2 zinc finger such that it CC binds to the S2 target subsite, and selecting the F3 zinc finger such CC that it binds to the S3 target subsite, thus designing (I) that binds to CC a target site. (I) is useful for recognition of triplet target subsites CC having the nucleotide G in the 5'-most position of the subsite. (I) is CC useful in studying gene function, and for human therapeutics and plant CC engineering. (I), (II) or (III) is useful in therapeutic methods to CC modulate the expression of a target region within a subject, in CC diagnostic methods for sequence specific detection of target nucleic acid CC in a sample, and in assays to determine the phenotype and function of

CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHILAR 7
 Db 1 RSDHILAR 7

RESULT 8

ABP48652
 ID ABP48652 standard; peptide; 7 AA.

AC ABP48652;

XX DT 28-AUG-2002 (first entry)

DB Zinc finger protein related peptide motif SEQ ID NO:894.

XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

XX PN WO200242459-A2.

XX PD 30-MAY-2002.

XX PR 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PT Liu Q;

XX DR WPI; 2002-500284/53.

XX DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
 gene function and for human therapeutics and plant engineering, comprises
 first, second and third zinc fingers, ordered from N- to C-terminus.

PT Example 1; Page 41; 81pp; English.

PT The present invention describes a zinc finger protein (I) that binds to a
 target site, comprising a first (F1), a second (F2), and a third (F3)
 zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 and a third (S3) target subsite. Also described are: (1) a polypeptide
 (II) comprising (I); (2) a poly nucleotide (III) encoding (I) or (II); and
 (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 binds to the S1 target subsite, selecting the F2 zinc finger such that it
 binds to the S2 target subsite, and selecting the F3 zinc finger such
 that it binds to the S3 target subsite, thus designing (I) that binds to
 a target site. (I) is useful for recognition of triplet target subsites
 having the nucleotide G in the 5'-most position of the subsite. (I) is
 useful in studying gene function, and for human therapeutics and plant
 engineering. (I), (II) or (III) is useful in therapeutic methods to
 modulate the expression of a target region within a subject, in
 diagnostic methods for sequence specific detection of target nucleic acid
 in a sample, and in assays to determine the phenotype and function of
 gene expression. (I) has improved affinity and specificity for their
 target sequences, as well as enhanced biological activity. ABQ71213 to
 ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 finger peptides which are given in the exemplification of the present
 invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHILAR 7
 Db 1 RSDHILAR 7

RESULT 9

ABP49518
 ID ABP49518 standard; peptide; 7 AA.

AC ABP49518;

XX DT 28-AUG-2002 (first entry)

DB Zinc finger protein related peptide motif SEQ ID NO:1748.

XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

XX PN WO200242459-A2.

XX PD 30-MAY-2002.

XX PR 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PT Liu Q;

XX DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
 gene function and for human therapeutics and plant engineering, comprises
 first, second and third zinc fingers, ordered from N- to C-terminus.

PT Example 1; Page 51; 81pp; English.

The present invention describes a zinc finger protein (I) that binds to a
 target site, comprising a first (F1), a second (F2), and a third (F3)
 zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 and a third (S3) target subsite. Also described are: (1) a polypeptide
 (II) comprising (I); (2) a poly nucleotide (III) encoding (I) or (II); and
 (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 binds to the S1 target subsite, selecting the F2 zinc finger such that it
 binds to the S2 target subsite, and selecting the F3 zinc finger such
 that it binds to the S3 target subsite, thus designing (I) that binds to
 a target site. (I) is useful for recognition of triplet target subsites
 having the nucleotide G in the 5'-most position of the subsite. (I) is
 useful in studying gene function, and for human therapeutics and plant
 engineering. (I), (II) or (III) is useful in therapeutic methods to
 modulate the expression of a target region within a subject, in
 diagnostic methods for sequence specific detection of target nucleic acid
 in a sample, and in assays to determine the phenotype and function of
 gene expression. (I) has improved affinity and specificity for their
 target sequences, as well as enhanced biological activity. ABQ71213 to
 ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 finger peptides which are given in the exemplification of the present
 invention

XX Sequence 7 AA;

CC invention

CC Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHILAR 7
 Db 1 RSDHILAR 7

RESULT 9

ABP49518
 ID ABP49518 standard; peptide; 7 AA.

AC ABP49518;

XX DT 28-AUG-2002 (first entry)

DB Zinc finger protein related peptide motif SEQ ID NO:1748.

XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

XX PN WO200242459-A2.

XX PD 30-MAY-2002.

XX PR 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PT Liu Q;

XX DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
 gene function and for human therapeutics and plant engineering, comprises
 first, second and third zinc fingers, ordered from N- to C-terminus.

PT Example 1; Page 51; 81pp; English.

The present invention describes a zinc finger protein (I) that binds to a
 target site, comprising a first (F1), a second (F2), and a third (F3)
 zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 and a third (S3) target subsite. Also described are: (1) a polypeptide
 (II) comprising (I); (2) a poly nucleotide (III) encoding (I) or (II); and
 (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 binds to the S1 target subsite, selecting the F2 zinc finger such that it
 binds to the S2 target subsite, and selecting the F3 zinc finger such
 that it binds to the S3 target subsite, thus designing (I) that binds to
 a target site. (I) is useful for recognition of triplet target subsites
 having the nucleotide G in the 5'-most position of the subsite. (I) is
 useful in studying gene function, and for human therapeutics and plant
 engineering. (I), (II) or (III) is useful in therapeutic methods to
 modulate the expression of a target region within a subject, in
 diagnostic methods for sequence specific detection of target nucleic acid
 in a sample, and in assays to determine the phenotype and function of
 gene expression. (I) has improved affinity and specificity for their
 target sequences, as well as enhanced biological activity. ABQ71213 to
 ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 finger peptides which are given in the exemplification of the present
 invention

XX Sequence 7 AA;

	Query Match	Match	Score	DB	Length	Y
	Best Local Similarity	100.0%	Score	5	7	X
	Matches	7	Pred. No.	1.7e+06		X
b	1 RSDHLAR	7				C
b	1 RSDHLAR	7				C
RESULT 10						
B	ABP49797					X
D	ABP49797 standard; peptide; 7 AA.					X
C	ABP49797;					X
X						X
X						X
X						X
X						X
T	28-AUG-2002 (first entry)					X
Zinc finger protein related peptide motif SEQ ID NO:2545.						X
Zinc finger protein; ZFP; DNA binding protein; zinc finger.						X
Homo sapiens.						X
Synthetic.						X
WO200242459-A2.						X
30-MAY-2002.						X
20-NOV-2001; 2001WO-US043438.						X
20-NOV-2000; 2000US-00716637.						X
(SANG-) SANGAMO BIOSCIENCES INC.						X
Liu Q;						X
WPI; 2002-500284/53.						X
New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.						X
Example 1; Page 54; 81pp; English.						X
The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ1213 to ABQ2214 and ABP48191 to ABP5230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.						X
Sequence 7 AA;						X
Query Match	100.0%	Score	7	DB	5	Length
Best Local Similarity	100.0%	Pred. No.	1.7e+06			Y
Matches	7	Mismatches	0	Indels	0	Gaps
Db	1 RSDHLAR					X
RESULT 11						
ABP48621						X
ID	ABP48621 standard; peptide; 7 AA.					X
AC	ABP48621;					X
XX						X
DT	28-AUG-2002 (first entry)					X
Zinc finger protein related peptide motif SEQ ID NO:679.						X
Zinc finger protein; ZFP; DNA binding protein; zinc finger.						X
Homo sapiens.						X
Synthetic.						X
PN	WO200242459-A2.					X
XX						X
PD	30-MAY-2002.					X
XX						X
PF	20-NOV-2001; 2001WO-US043438.					X
XX						X
PR	20-NOV-2000; 2000US-00716637.					X
XX						X
PA	(SANG-) SANGAMO BIOSCIENCES INC.					X
XX						X
PI	Liu Q;					X
DR	WPI; 2002-500284/53.					X
XX						X
PT	New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.					X
XX						X
PS	Example 1; Page 41; 81pp; English.					X
XX						X
The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ1213 to ABQ2214 and ABP48191 to ABP5230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.						X
Sequence 7 AA;						X

RESULT 12
 XX ABP49260
 ID ABP49260 standard; peptide; 7 AA.
 XX
 AC
 XX DT 28-AUG-2002 (first entry)
 XX DE Zinc finger protein related peptide motif SEQ ID NO:1388.
 XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200242459-A2.
 XX PD 30-MAY-2002.
 XX PR 20-NOV-2001; 2001WO-US043438.
 XX PA 20-NOV-2000; 2000US-00716637.
 XX PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX PI Liu Q;
 XX PT New zinc finger protein that binds to target site, useful in studying PT gene function and for human therapeutics and plant engineering, comprises PT first, second and third zinc fingers, ordered from N- to C-terminus.
 XX PS Example 1; Page 48; 81pp; English.
 XX PT New zinc finger protein that binds to target site, useful in studying PT gene function and for human therapeutics and plant engineering, comprises PT first, second and third zinc fingers, ordered from N- to C-terminus.
 XX PS Example 1; Page 56; 81pp; English.
 XX PT The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a poly nucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ1213 to ABQ2214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSDHLAR 7
 Db 1 RSDHLAR 7
 RESULT 14
 ABP48649
 ID ABP48649 standard; peptide; 7 AA.
 XX AC ABP48649;
 XX DT 28-AUG-2002 (first entry)

RESULT 13
 ABP50082 standard; peptide; 7 AA.
 ID ABP50082

XX
DE zinc finger protein related peptide motif SEQ ID NO:893.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
OS Homo sapiens.
OS Synthetic.
XX
W0200242459-A2.
XX
PD 30-MAY-2002.
XX
PP 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PT Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 41; 8lpp; English.
XX
The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M). (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABP72214 and ABP8191 to ABP5120 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
XX
Sequence 7 AA:
SQ Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSDHLAR 7
Db 1 RSDHLAR 7
RESULT 15
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSDHLAR 7
Db 1 RSDHLAR 7
Search completed: December 27, 2004, 18:06:43
Job time : 67.75 secs

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OM protein - protein search, using sw model

Run on:

December 27, 2004, 17:02:31 ; Search time 15.8 Seconds

(without alignments)

29.381 Million cell updates/sec

Title: US-09-846-033B-34

Perfect score: 7

Sequence: 1 RSDHLAR 7

Scoring table: OLIGO

Gapop 60.0 , Gapext: 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA,*

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1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcmUS-COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	7	100.0	7	4 US-09-779-233-42
2	7	100.0	100	4 US-09-248-796A-16192

ALIGNMENTS

```

RESULT 1
US-09-779-233-42
; Sequence 42, Application US/09779233
; Patent No. 668958
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-010
; CURRENT APPLICATION NUMBER: US/09/779, 233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 42
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recognition
; OTHER INFORMATION: helix
US-09-779-233-42
```

Query Match	Score	DB	Length	7;	100.0%;	Score	7;	DB	4;	Length	7;										
Best Local Similarity	100.0%	Pred.	No.	3.8e+05;	Mismatches	0;	Indels	0;	Gaps	0;	Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	1	RSDHLAR	7																		
Db	1	RSDHLAR	7																		

RESULT 2

US-09-248-796A-16192

Sequence 16192, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074, 725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096, 409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO: 16192

LENGTH: 100

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-16192

Query Match

100.0%; Score 7; DB 4; Length 100;

Best Local Similarity 100.0%; Pred. No. 0.23; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 RSDHLAR 7

Db

57 RSDHLAR 63

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On protein - protein search, using SW model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 seconds
(without alignments)
28.393 Million cell updates/sec

Title: US-09-846-033B-99
Perfect score: 7
Sequence: 1 RSDALRQ 7

Scoring table: OLIGO

Gapop 60.0 , Gapext: 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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Issued Patients AA:*
1: /cgnd_6/prodata/1/jaa/5A_COMB_pep:*
2: /cgnd_6/prodata/1/jaa/5B_COMB_pep:*
3: /cgnd_6/prodata/1/jaa/6A_COMB_pep:*
4: /cgnd_6/prodata/1/jaa/6B_COMB_pep:*
5: /cgnd_6/prodata/1/jaa/PCNTUS_COMB_pep:*
6: /cgnd_6/prodata/1/jaa/backfFile1_pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match Length	DB ID	Description
-----	-----	-----	-----

No matches found

Search completed: December 27, 2004, 21:40:38
Job time : 17.35 sec

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OM protein - protein search, using SW model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds
 (without alignments)
 29.289 Million cell updates/sec

Title: US-09-846-033B-98
 Perfect score: 7
 Sequence: 1 RSDALAR 7

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 478139 SEQB, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/prodata1/iaa/5A_COMB.pep:*

2: /cgn2_6/prodata1/iaa/5B_COMB.pep:*

3: /cgn2_6/prodata1/iaa/6A_COMB.pep:*

4: /cgn2_6/prodata1/iaa/6B_COMB.pep:*

5: /cgn2_6/prodata1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/prodata1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	7	100.0	881 3	US-09-413-814-44 Sequence 44, Appl

ALIGNMENTS

RESULT 1
 US-09-413-814-44
 Sequence 44, Application US/09413814
 ; Sequence 44, Application US/09413814
 ; Patent No. 6225064
 ; GENERAL INFORMATION:
 ; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 ; APPLICANT: Bristol-Myers Squibb, Co.
 ; APPLICANT: Beyer, Stefan
 ; APPLICANT: Bloecker, Helmut
 ; APPLICANT: Brandt, Peter
 ; APPLICANT: Cino, Paul M
 ; APPLICANT: Dougherty, Brian A
 ; APPLICANT: Goldberg, Steven L
 ; APPLICANT: Hofle, Gerhard
 ; APPLICANT: Mueller, Joachim
 ; APPLICANT: Reichenbach, Hans
 ; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
 ; TITLE OF INVENTION: heteropolyketide compounds
 ; FILE REFERENCE: PCT/US 99/23535
 ; CURRENT FILING NUMBER: US/09/413,814
 ; CURRENT FILING DATE: 1999-10-07

Query Match length: 881 ;
 Score 7; DB 3; Length 881;
 Best Local Similarity 100%; Pred. No. 6; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RSDALAR 7
 Db 295 RSDALAR 301

Search completed: December 27, 2004, 20:31:05
 Job time : 16.85 secs

; EARLIER APPLICATION NUMBER: DE 198 46 493.2
 ; EARLIER FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 44
 ; LENGTH: 881
 ; TYPE: PRT
 ; ORGANISM: Sorangium cellulosum
 US-09-413-814-44

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OM protein - protein search, using SW model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 seconds
(without alignments)
29.289 Million cell updates/sec

Title: US-09-846-033B-97

Perfect score: 7

Sequence: 1 QSGSLTR 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Issued Patents Av.*

1: /cgn2_6_ptodata/1/1aa/5A_COMB.pep:*
 2: /cgn2_6_ptodata/1/1aa/5B_COMB.pep:*
 3: /cgn2_6_ptodata/1/1aa/6A_COMB.pep:*
 4: /cgn2_6_ptodata/1/1aa/6B_COMB.pep:*
 5: /cgn2_6_ptodata/1/1aa/PCetus_COMB.pep:*
 6: /cgn2_6_ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	7	100.0	7	US-09-731-558-16
				Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-731-558-16
Sequence 16, Application US/09731558
; Patent No. 6503717
; GENERAL INFORMATION:
; APPLICANT: Case, Casey Christopher
; APPLICANT: Liu, Qiang
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
; TITLE OF INVENTION: Proteins for the Identification of Gene Function
; FILE REFERENCE: 019496-003210US
; CURRENT APPLICATION NUMBER: US/09/731,558
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 09/456,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SB5
; OTHER INFORMATION: recognition helix
US-09-731-558-16

Qy	1 QSGSLTR 7	Db	1 QSGSLTR 7
Query Match	100.0%	Score	7;
Best Local Similarity	100.0%	DB	4;
Matches	7;	Length	7;
		Pred. No.	3.8e+05;
		Mismatches	0;
		Indels	0;
		Gaps	0;

Search completed: December 27, 2004, 20:31:04
Job time : 15.85 secs

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OM protein - protein search, using SW model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds
 (without alignments)
 29.289 Million cell updates/sec

Title: US-09-846-033B-96

Perfect score: 7

Sequence: 1 RSDALSA 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgnd_6/prodata/1/1aa/5A_COMBO.pep:*

2: /cgnd_6/prodata/1/1aa/5B_COMBO.pep:*

3: /cgnd_6/prodata/1/1aa/63_COMBO.pep:*

4: /cgnd_6/prodata/1/1aa/68_COMBO.pep:*

5: /cgnd_6/prodata/1/1aa/PCUTS_COMBO.pep:*

6: /cgnd_6/prodata/1/1aa/backfilesl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
------------	-------------	--------	-------	-------------

No matches found

Search completed: December 27, 2004, 20:31:04
 Job time : 15.85 secB

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds

(without alignments)

29.289 Million cell updates/sec

Title: US-09-846-0338-95

Perfect score: 7 RESULT 7

Scoring table: OutGO GapOp 60.0 , Gapext 60.0

Searched: 478139 seqB, 63318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 59

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/pctodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/pctodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/pctodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/pctodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/pctodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/pctodata/1/iaa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	7	100.0	7 4 US-09-014-679A-19	Sequence 19, Appl
2	7	100.0	10 3 US-09-139-762A-19	Sequence 19, Appl
3	7	100.0	10 3 US-09-139-762A-53	Sequence 53, Appl
4	7	100.0	20 1 US-08-040-534-19	Sequence 19, Appl
5	7	100.0	20 1 US-08-040-534-19	Sequence 19, Appl
6	7	100.0	21 4 US-09-0229-007A-95	Sequence 95, Appl
7	7	100.0	21 4 US-10-013-424-95	Sequence 95, Appl
8	7	100.0	26 1 US-08-020-151-11	Sequence 111, Appl
9	7	100.0	28 1 US-08-040-538-34	Sequence 34, Appl
10	7	100.0	28 1 US-08-066-44-34	Sequence 34, Appl
11	7	100.0	28 3 US-09-058-459-1	Sequence 1, Appl
12	7	100.0	28 3 US-09-027-956-1	Sequence 1, Appl
13	7	100.0	28 3 US-09-037-179B-15	Sequence 15, Appl
14	7	100.0	28 4 US-09-240-179-2	Sequence 1, Appl
15	7	100.0	28 4 US-09-014-357-1	Sequence 1, Appl
16	7	100.0	28 4 US-09-500-00-70	Sequence 70, Appl
17	7	100.0	28 4 US-09-716-637-13	Sequence 13, Appl
18	7	100.0	59 1 US-08-040-548-7	Sequence 7, Appl
19	7	100.0	59 1 US-08-246-44-7	Sequence 8, Appl
20	7	100.0	85 4 US-09-229-007A-8	Sequence 8, Appl
21	7	100.0	85 4 US-10-013-424-8	Sequence 8, Appl
22	7	100.0	86 6 520615-3	Patent No. 5206152
23	7	100.0	87 4 US-10-057-552-1	Sequence 1, Appl
24	7	100.0	89 1 US-08-040-548-8	Sequence 8, Appl
25	7	100.0	89 1 US-08-166-344-8	Sequence 8, Appl
26	7	100.0	91 3 US-08-863-813A-5	Sequence 5, Appl
27	7	100.0	91 3 US-08-676-318A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-614-679A-19

; Sequence 19, Application US/09614679A

; Patent No. 6492117

; GENERAL INFORMATION:

; APPLICANT: CHOO, YEN

; APPLICANT: PATEL, SACHIN

; APPLICANT: BALASUBRAMANIAN, SHANKAR

; APPLICANT: LIU, XIAOHAI

; TITLE OF INVENTION: MOLECULES

; FILE REFERENCE: 71278/271599

; CURRENT FILING DATE: 2000-07-12

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide

RESULT 2
US-09-614-679A-19

Query Match

Best Local Similarity 100.0%; Score 7; DB 4; Length 7; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy	1 RSDHLLT 7	Db	1 RSDHLLT 7

; GENERAL INFORMATION:

; APPLICANT: Choo, Yen

; APPLICANT: Klug, Aaron

; APPLICANT: Sanchez Garcia, Isidro

; TITLE OF INVENTION: Improvements in or Relating to

; TITLE OF INVENTION: Binding Proteins for Recognition of DNA

; NUMBER OF SEQUENCES: 125

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

; STREET: 1100 New York Avenue, N.W.

; CITY: Washington

; STATE: D.C.

COUNTRY: USA
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect
 CURRENT APPLICATION DATA:
 FILING DATE:
 PRIORITY CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/793,408
 FILING DATE: 02-JUN-1997
 APPLICATION NUMBER: PCT/GB95/01949
 FILING DATE: 17-AUG-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/139,762A
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9514698.1
 FILING DATE: 18-JUL-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9422534.9
 FILING DATE: 08-NOV-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9416880.4
 FILING DATE: 20-AUG-1994
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-09-139-762A-19

Query Match 100.0%; Score 7; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.017; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RSDHLLT 7	1 RSDHLLT 7
Db		

RESULT 3
 US-09-139-762A-53
 Sequence 53, Application US/09139762A
 ;
 ; GENERAL INFORMATION:
 ; PATENT NO. 6013653
 ;
 ; APPLICANT: Choo, Yen
 ;
 ; APPLICANT: Klug, Aaron
 ;
 ; APPLICANT: Sanchez Garcia, Isidro
 ;
 ; TITLE OF INVENTION: Improvements in or Relating to
 ;
 ; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
 ;
 ; NUMBER OF SEQUENCES: 125
 ;
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Arnold, White & Durkee
 ;
 ; STREET: 321 No. 5763209th Clark Street, Suite 800
 ;
 ; CITY: Chicago
 ;
 ; STATE: Illinois
 ;
 ; COUNTRY: U.S.A.
 ;
 ; ZIP: 60610
 ;
 ; COMPUTER READABLE FORM:
 ;
 ; MEDIUM TYPE: Floppy disk
 ;
 ; COMPUTER: IBM PC compatible
 ;
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ;
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ;
 ; APPLICATION NUMBER: US/08/040,548
 ;
 ; FILING DATE:
 ;
 ; CLASSIFICATION: 514
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ;
 ; NAME: Coughlin, Daniel F.
 ;
 ; REGISTRATION NUMBER: 36,111
 ;
 ; REFERENCE/DOCKET NUMBER: arcd067
 ;
 ; TELECOMMUNICATION INFORMATION:
 ;
 ; TELEPHONE: (312) 744-0030
 ;
 ; TELEFAX: (312) 245-4961
 ;
 ; INFORMATION FOR SEQ ID NO: 19:
 ;
 ; SEQUENCE CHARACTERISTICS:
 ;
 ; LENGTH: 20 amino acids
 ;
 ; TYPE: amino acid
 ;
 ; STRANDEDNESS: single
 ;
 ; TOPOLOGY: linear
 ;
 ; MOLECULE TYPE: peptide
 ;
 ; US-08-040-548-19

Query Match 100.0%; Score 7; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.031; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-08-040-548-19
 Sequence 19, Application US/08040548
 ;
 ; PATENT NO. 5762209
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Sukhatme, Vikas P.
 ;
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
 ;
 ; NUMBER OF SEQUENCES: 67
 ;
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Arnold, White & Durkee
 ;
 ; STREET: 321 No. 5763209th Clark Street, Suite 800
 ;
 ; CITY: Chicago
 ;
 ; STATE: Illinois
 ;
 ; COUNTRY: U.S.A.
 ;
 ; ZIP: 60610
 ;
 ; COMPUTER READABLE FORM:
 ;
 ; MEDIUM TYPE: Floppy disk
 ;
 ; COMPUTER: IBM PC compatible
 ;
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ;
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ;
 ; APPLICATION NUMBER: US/08/040,548
 ;
 ; FILING DATE:
 ;
 ; CLASSIFICATION: 514
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ;
 ; NAME: Coughlin, Daniel F.
 ;
 ; REGISTRATION NUMBER: 36,111
 ;
 ; REFERENCE/DOCKET NUMBER: arcd067
 ;
 ; TELECOMMUNICATION INFORMATION:
 ;
 ; TELEPHONE: (312) 744-0030
 ;
 ; TELEFAX: (312) 245-4961
 ;
 ; INFORMATION FOR SEQ ID NO: 19:
 ;
 ; SEQUENCE CHARACTERISTICS:
 ;
 ; LENGTH: 20 amino acids
 ;
 ; TYPE: amino acid
 ;
 ; STRANDEDNESS: single
 ;
 ; TOPOLOGY: linear
 ;
 ; MOLECULE TYPE: peptide
 ;
 ; US-08-040-548-19

Qy 1 RSDHLLT 7
 Qy 9 RSDHLLT 15
 Db
 ;
RESULT 5
 US-08-466-344-19
 ; Sequence 19, Application US/08466344
 ; Patent No. 5773583
 ; GENERAL INFORMATION:
 ; APPLICANT: Sukhatme, Vikas P.
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
 ; NUMBER OF SEQUENCES: 67
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: 321 NO. 5773583th Clark Street, Suite 800
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60610
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Pattern Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08466,344
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/040,548
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coughlin, Daniel F.
 ; REGISTRATION NUMBER: 36,111
 ; REFERENCE/DOCKET NUMBER: arcd067
 ; TELEPHONE: (312) 744-0090
 ; TELEFAX: (312) 245-4961
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-466-344-19
 ; Query Match 100.0%; Score 7; DB 1; Length 20;
 ; Best Local Similarity 100.0%; Pred. No. 0.031; Mismatches 0;
 ; Matches 7; Conservative 0; Indels 0; Gaps 0;
 ; Qy 1 RSDHLLT 7
 ; Qy 9 RSDHLLT 15
 ; Db
 ;
RESULT 6
 US-09-229-007A-95
 ; Sequence 95, Application US/09229007A
 ; Patent No. 6453242
 ; GENERAL INFORMATION:
 ; APPLICANT: Eisenberg, Stephen P.
 ; APPLICANT: Case, Casey C.
 ; APPLICANT: Cox III, George N.
 ; APPLICANT: Jamieson, Andrew
 ; APPLICANT: Rebar, Edward J.
 ; APPLICANT: Sangamo Biosciences, Inc.
 ; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger Proteins
 ; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
 ; TITLE OF INVENTION: to Bind to Presellected SiteS
 ; FILE REFERENCE: 019496-001800US
 ; CURRENT APPLICATION NUMBER: US10/113,424
 ; CURRENT FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: US/09/229,007A
 ; PRIOR FILING DATE: 1999-01-12
 ; NUMBER OF SEQ ID NOS: 97
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 95
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence
 ; OTHER INFORMATION: (F1, F2 and F3) from Zif 268
 ; US-10-113-424-95
 ; Query Match 100.0%; Score 7; DB 4; Length 21;
 ; Best Local Similarity 100.0%; Pred. No. 0.033; Mismatches 0;
 ; Matches 7; Conservative 0; Indels 0; Gaps 0;
 ; Qy 1 RSDHLLT 7
 ; Qy 9 RSDHLLT 15
 ; Db
 ;
RESULT 8
 US-08-620-151-111
 ; Sequence 111, Application US/08620151
 ; Patent No. 5928955
 ; GENERAL INFORMATION:
 ; APPLICANT: Imperiale, Barbara
 ; APPLICANT: Walko, Grant K.
 ; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
 ; TITLE OF INVENTION: DIVALENT ZINC
 ; NUMBER OF SEQUENCES: 136
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
 STREET: NBC Tower - Suite 3600, 455 N. Cityfront
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60611-5599

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/620,151
 FILING DATE: 22-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Shaanon, Karen L.
 REGISTRATION NUMBER: 36,675
 REFERENCE/DOCKET NUMBER: 8597/6

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-321-4200
 TELEFAX: 312-321-4299

SEQUENCE CHARACTERISTICS:
 LENGTH: 26 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-620-151-111

Query Match 100.0%; Score 7; DB 2; Length 26;
 Best local Similarity 100.0%; Pred. No. 0.04; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 RSDHLLT 7
 Db 9 RSDHLLT 15

RESULT 10
 US-08-466-344-34
 Sequence 34, Application US/08466344
 Patent No. 5773583

GENERAL INFORMATION:
 APPLICANT: Sukhatme, Vikas P.
 TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
 TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
 NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: 321 No. 5773583th Clark Street, Suite 800
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,344
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/040,548
 FILING DATE: 31-MAR-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Coughlin, Daniel F.
 REGISTRATION NUMBER: 36,111
 REFERENCE/DOCKET NUMBER: arcd067

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 744-0090
 TELEFAX: (312) 245-4961

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-08-466-344-34

Query Match 100.0%; Score 7; DB 1; Length 28;
 Best local Similarity 100.0%; Pred. No. 0.043; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 RSDHLLT 7
 Db 9 RSDHLLT 15

RESULT 11
 US-09-058-459-1

```

; Sequence 1, Application US/09058459
; Patent No. 618895
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Gordon, D. B.
; APPLICANT: Street, Arthur
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
; FILE REFERENCE: A6553-3/RFT/RMS/SIR
; CURRENT APPLICATION NUMBER: US/09/058, 459
; CURRENT FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/043, 464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054, 678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061, 097
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
US-09-058-459-1.

RESULT 12
; Sequence 1, Application US/09127926
; Patent No. 6229312
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Gordon, D. Benjamin
; APPLICANT: Street, Arthur
; APPLICANT: Su, Yaoying
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
; FILE REFERENCE: A65353-4/RFT/RMS/SIR
; CURRENT APPLICATION NUMBER: US/09/127, 926
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/043, 464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054, 678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061, 097
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: 09/058, 459
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/087, 561
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
US-09-127-926-1.

Query Match          100.0%; Score 7; DB 3; Length 28;
Best Local Similarity      100.0%; Pred. No. 0.043; Mismatches 0; Indels 0; Gaps 0;
Matches    7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RSDHITT 7
Db      14 RSDHITT 20

RESULT 13
; Sequence 15, Application US/09037179B
; Patent No. 631659
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the Wilms' Tumor Gene
; FILE REFERENCE: 0050-1312-011
; CURRENT APPLICATION NUMBER: US/09/037, 179B
; CURRENT FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102, 942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614, 161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435, 780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795, 323
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-037-179B-15

RESULT 14
; Sequence 2, Application US/09240179
; Patent No. 6410248
; GENERAL INFORMATION:
; APPLICANT: Greszman, Harvey A.
; APPLICANT: Pabo, Carl O.
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc Finger Proteins for Diverse DNA Target Sites
; FILE REFERENCE: 01996-000220US
; CURRENT APPLICATION NUMBER: US/09/240,179
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 60/073, 223
; EARLIER FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Zif268 zinc
; OTHER INFORMATION: finger 2
; OTHER INFORMATION: finger 2
US-09-240-179-2

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Query Match 100.0%; Score 7; DB 4; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.043; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RSDHLTT 7 Db	13 RSDHLTT 19
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RESULT 15
 US-09-714-357-1
 ; Sequence 1, Application US/09714357
 ; Patent No. 6708120
 ; GENERAL INFORMATION:
 ; APPLICANT: Mayo, Stephen L.
 ; APPLICANT: Dahiya, Basil I.
 ; APPLICANT: Gordon, D. B.
 ; APPLICANT: Street, Arthur
 ; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
 ; FILE REFERENCE: A65353-2/RFTRMS/SJR
 ; CURRENT APPLICATION NUMBER: US/09/714,357
 ; CURRENT FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: 09/058,459
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: 60/054,678
 ; PRIOR FILING DATE: 1997-08-04
 ; PRIOR APPLICATION NUMBER: 60/061,097
 ; PRIOR FILING DATE: 1997-10-03
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ_ID NO 1
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Mouse
 US-09-714-357-1

Query Match 100.0%; Score 7; DB 4; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.043; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RSDHLTT 7 Db	14 RSDHLTT 20
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Search completed: December 27, 2004, 20:31:04
 Job time : 15.85 secs